RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/018,716

Source: T-W-16-4

Date Processed by STIC: 12-22-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
   U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: 10/018,716

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1.____ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2.____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3.____ Misaligned Amino Numbering — The numbering under each 5ᵗʰ amino acid is misaligned. Do not use tab codes between numbers: use space characters, instead.

4.____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5.____ Variable Length — Sequence(s)____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6.____ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section from the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7.____ Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8.____ Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9.____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10.____ Invalid <211> Response — Per 1.823 of Sequence Rules, the only valid <211> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <211> response is Unknown or is Artificial Sequence

11.____ Use of <220> — Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses
Use of <220> to <223> is MANDATORY if <211> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12.____ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13.____ Misuse of n/Xaa — "n" can only represent a single nucleotide: "Xaa" can only represent a single amino acid

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          RAW SEQUENCE LISTING             DATE: 12/22/2004
          PATENT APPLICATION:  US/10/018,716    TIME: 13:15:56

          Input Set : N:\FATIMA\10018716.txt
          Output Set: N:\CRF4\12222004\J018716.raw

     4 <110> APPLICANT: Labarbera, Andrew
     5         Wang, YiFang
     6         Zhu, ChangHong
     8 <120> TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES FOR FERTILITY
     9         AND MENSTRUAL CYCLE REGULATION AND FOR CHEMOPREVENTIVE AND
    10         CHEMOTHERAPEUTIC USE
    12 <130> FILE REFERENCE: 91830/0476600
    14 <140> CURRENT APPLICATION NUMBER: 10/018,716
C-->15 <141> CURRENT FILING DATE: 2002-03-28
    17 <150> PRIOR APPLICATION NUMBER: 60/136,489
    18 <151> PRIOR FILING DATE: 1999-05-28
    20 <150> PRIOR APPLICATION NUMBER: 60/158,612
    21 <151> PRIOR FILING DATE: 1999-10-08
    23 <150> PRIOR APPLICATION NUMBER: US00/13488
    24 <151> PRIOR FILING DATE: 2000-05-16
    26 <160> NUMBER OF SEQ ID NOS: 4
    28 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    30 <210> SEQ ID NO: 1
    31 <211> LENGTH: 18
    32 <212> TYPE: DNA
    33 <213> ORGANISM: Nucleic Acid
    35 <400> SEQUENCE: 1
    36 gagcagggcc ataattat
    38 <210> SEQ ID NO: 2
    39 <211> LENGTH: 18
    40 <212> TYPE: RNA
    41 <213> ORGANISM: Nucleic Acid
    43 <400> SEQUENCE: 2
    44 auaauuaugg cccugcuc
    46 <210> SEQ ID NO: 3
    47 <211> LENGTH: 18
    48 <212> TYPE: DNA
    49 <213> ORGANISM: Nucleic Acid
    51 <400> SEQUENCE: 3
    52 gagcaaggac atgattat
    54 <210> SEQ ID NO: 4
    55 <211> LENGTH: 18
    56 <212> TYPE: RNA
    57 <213> ORGANISM: Nucleic Acid
    59 <400> SEQUENCE: 4
    60 auaaugaugu ccuugcuc
```

Handwritten annotations:

Does Not Comply
Corrected Diskette Needed
(pg.1)

Invalid Response (×4)

← Mandatory

18 <213> response

18 has to be either Artificial Unknown or Genus/Species.

See item #10 on error summary sheet.

12/22/04

VERIFICATION SUMMARY   DATE: 12/22/2004
PATENT APPLICATION: US/10/018,716   TIME: 13:15:57

Input Set : N:\FATIMA\10018716.txt
Output Set: N:\CRF4\12222004\J018716.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date